

TECHNICAL AMENDMENTS TO THE CLAIMS:

Please cancel Claims 1-5, 17-23, and 29-30 without disclaimer or prejudice to Applicants' right to pursue the subject matter of these claims in a future divisional or continuation application.

Please amend Claims 6-16, 24-28 and 31-32 to read as follows:

1. (Cancelled)
2. (Cancelled)
3. (Cancelled)
4. (Cancelled)
5. (Cancelled)
6. (Newly Amended) ~~The A nucleic acid fragment comprising an inducible plant class II o-methyltransferase (COMT II) gene promoter isolated from as claimed in claim 5, characterized in that the plant is a dicotyledonous plant, preferably tobacco.~~
7. (Newly amended) ~~The nucleic acid fragment as claimed in one of Claims 1 to 6, wherein characterized in that the COMT II promoter comprises nucleic acids a sequence in 5' upstream of the translation initiation site, or start codon (ATG) of the coding region sequence of the tobacco COMT II gene, said upstream nucleic acids which allowsing the transcription and the expression of said coding region sequence.~~
8. (Newly amended) ~~The nucleic acid fragment as claimed in of Celaim 1 to 7, wherein characterized in that the COMT II promoter comprises a sequence of more than 600 nucleotides upstream of the COMT II gene translation initiation site ATG, preferably more than 1 000 nucleotides~~

~~upstream of the ATG, more preferentially of more than 1-200 nucleotides upstream of the ATG.~~

9. (Newly amended) The nucleic acid ~~fragment as claimed in one of~~ Claims 1 to 8, wherein characterized in that the COMT II promoter comprises a transcription initiation site located less than 100 nucleotides upstream of the COMT II gene translation initiation site ATG, ~~advantageously approximately 90 nucleotides upstream.~~

10. (Newly amended) The nucleic acid ~~fragment as claimed in one of~~ Claims 1 to 9, wherein characterized in that the 3' end of the promoter is located between the transcription initiation site and the translation initiation site of the COMT II gene ATG.

11. (Newly amended) The nucleic acid ~~fragment as claimed in~~ of Claim 10, wherein characterized in that the 3' end of the promoter is located between 10 and 50 nucleotides downstream of the transcription initiation site, ~~more preferentially between 20 and 40 nucleotides downstream, even more preferentially between 20 and 30 nucleotides downstream.~~

12. (Newly amended) The nucleic acid ~~fragment as claimed in one of~~ Claims 1 to 11, wherein characterized in that it said nucleic acid comprises ~~eonsists of~~ the tobacco COMT II promoter ~~defined by the nucleotide sequence upstream of the ATG represented by sequence identifier 1 (of SEQ ID NO:1), the sequences~~ nucleic acids capable of hybridizing selectively to said sequence SEQ ID NO:1, and nucleic acids ~~the homologous to~~ SEQ ID NO:1 ~~sequences.~~

13. (Newly amended) The nucleic acid ~~fragment as claimed in~~ of Claim 12, wherein characterized in that it said nucleic acid comprises ~~eonsists of~~ the sequence between nucleotides 557 and 1796 of SEQ ID NO:1 ~~sequence identifier No. 1.~~

14. (Newly amended) A chimeric gene ~~(or expression cassette)~~ which is functional in plant

~~cells and the plants comprising, in the direction of transcription, a nucleic acid comprising a 5' regulatory region sequence which is functional in plant cells in 5', a nucleic acid encoding sequence a protein which is functional in plant cells, and a nucleic acid comprising a 3' regulatory region sequence in 3' which is functional in plant cells, characterized in that wherein the 5' regulatory region sequence in 5' comprises the nucleic acid fragment as claimed in one of any one of Claims 1 to 6, 7, 8, 9, 10, 11, 12 and 13.~~

15. (Newly amended) The chimeric gene as claimed in of Claim 14, wherein characterized in that the coding sequence comprises a coding sequence for a reporter gene or a coding sequence for protein encoded by said nucleic acid encoding a protein which is functional in plant cells is a reporter protein or a protein of interest which is functional in plant cells.

16. (Newly amended) The chimeric gene as claimed in of Claims 15, wherein characterized in that the protein of interest which is functional in plant cells is a protein which confers onto the plants cells resistance to infestation by diseases or to insects.

17. (Cancelled)

18. (Cancelled)

19. (Cancelled)

20. (Cancelled)

21. (Cancelled)

22. (Cancelled)

23. (Cancelled)

24. (Newly amended) A ~~cloning and/or expression~~ vector for transforming plant cells or plants, characterized in that it contains at least one comprising the chimeric gene as claimed in of Claims 14 to 23.

25. (Newly amended) A method for transforming plant cells, characterized in that it consists in comprising integrating into the genome of said plant cells the at least one chimeric gene as claimed in one of Claims 14 to 23.

26. (Newly amended) A transformed plant cell, characterized in that it comprises the a chimeric gene as claimed in of Claims 14 to 23.

27. (Newly amended) A transformed plant, characterized in that it comprises the a chimeric gene as claimed in of Claims 14 to 23.

28. (Newly amended) A plant, characterized in that it contains comprising the transformed cells as claimed in of Claim 26 or obtained using the method as claimed in of Claim 25.

29. (Cancelled)

30. (Cancelled)

31. (Newly amended) The plant as claimed in one of any one of Claims 27 and 28 to 30, wherein said plant characterized in that it is one of the a monocotyledonous plant monocotyledon type, in particular a cereal, sugar cane, rice or maize, or of the dicotyledon type, in particular tobacco, soybean, rapeseed, cotton, sunflower, beetroot or clover.

32. (Newly amended) A grain obtained from the of plants as claimed in one of any one of Claims 27 28, 31 and 40 to 34.

Please add the following new claims:

33. (New) The nucleic acid of Claim 6, wherein the dicotyledonous plant is a tobacco plant.
34. (New) The nucleic acid of Claim 7, wherein the COMT II promoter comprises more than 1,000 nucleotides upstream of the COMT II gene translation initiation site.
34. (New) The nucleic acid of Claim 7, wherein the COMT II promoter comprises more than 1,200 nucleotides upstream of the COMT II gene translation initiation site.
35. (New) The nucleic acid of Claim 7, wherein the COMT II promoter comprises more than 1,800 nucleotides upstream of the COMT II gene translation initiation site.
36. (New) The nucleic acid of Claim 7, wherein the COMT II promoter is the nucleic acid of SEQ ID NO:1.
37. (New) The nucleic acid of Claim 8, wherein the COMT II promoter comprises a transcription initiation site located less than 100 nucleotides upstream of the COMT II gene translation initiation site.
38. (New) The nucleic acid of Claim 10, wherein the 3' end of the promoter is located between 20 and 40 nucleotides downstream of the transcription initiation site.
39. (New) The nucleic acid of Claim 10, wherein the 3' end of the promoter is located between 20 and 30 nucleotides downstream of the transcription initiation site.
40. (New) The plant of Claim 31, wherein said monocotyledonous plant is selected from the group consisting of cereal, sugar cane, rice or maize.
41. (New) The plant of any one of Claims 27 and 28, wherein said plant is a dicotyledonous

plant.

42. (New) The plant of Claim 41, wherein said dicotyledonous plant is selected from the group consisting of tobacco, soybean, rapeseed, cotton, sunflower, beetroot or clover.